

We claim:

1. An isolated nucleic acid sequence which encodes a polypeptide
5 and which is composed of a combination of the nucleic acid
sequences of a biosynthesis nucleic acid sequence of the
fatty acid or lipid metabolism and one of the following
nucleic acids:
 - 10 a) a nucleic acid sequence with the sequence shown in SEQ ID
NO: 1,
 - b) nucleic acid sequences which are derived from the nucleic
acid sequence shown in SEQ ID NO: 1 as the result of the
15 degeneracy of the genetic code,
 - c) derivatives of the nucleic acid sequence shown in SEQ ID
NO: 1 which encode polypeptides with the amino acid
sequences shown in SEQ ID NO: 2 and which have at least
20 60% homology at the amino acid level,
 - d) a nucleic acid sequence with the sequence shown in SEQ ID
NO: 3 or the amino-terminal portion of the coding region
of this sequence.
- 25 2. An isolated nucleic acid sequence as claimed in claim 1,
wherein a sequence of the following protein groups is used as
biosynthesis gene nucleic acid sequence of the fatty acid or
lipid metabolism:
30 Acyl-CoA dehydrogenase(s), Acyl-ACP [= acyl carrier protein]
desaturase(s), Acyl-ACP thioesterase(s), fatty acid
acyltransferase(s), fatty acid synthase(s), fatty acid
hydroxylase(s), acetyl-coenzyme A carboxylase(s),
acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty
35 acid acetylenases, lipxygenases, triacylglycerol lipases,
allenoxy synthases, hydroperoxide lyases and/or fatty acid
elongase(s).
3. An isolated nucleic acid sequence as claimed in claim 1 or 2,
40 wherein a sequence of the following protein groups is used as
biosynthesis gene nucleic acid sequence of the fatty acid or
lipid metabolism:
fatty acid acyltransferase(s), $\Delta 4$ desaturase, $\Delta 5$ desaturase,
 $\Delta 6$ desaturase, $\Delta 9$ desaturase, $\Delta 12$ desaturase, $\Delta 15$ desaturase
45 or a fatty acid elongase.

4. An isolated nucleic acid sequence as claimed in any of claims 1 to 3, wherein the derivatives mentioned under (c) have a homology at the amino acid level of 70%, preferably 80%, especially preferably of 90%, over the entire region of the sequence shown in SEQ ID NO: 2 (Program PileUp, J. Mol. Evolution., 25, 351-360, 1987, Higgins et al., CABIOS, 5 1989: 151-153).
5. An amino acid sequence encoded by a nucleic acid sequence as claimed in claim 1.
6. A nucleic acid construct comprising a nucleic acid sequence as claimed in claim 1, wherein the nucleic acid sequence is linked to one or more regulatory signals.
7. The use of a nucleic acid sequence as claimed in claim 1 or of a nucleic acid construct as claimed in claim 6 for the generation of transgenic plants.
8. A vector comprising a nucleic acid sequence as claimed in claim 1 or a nucleic acid construct as claimed in claim 6.
9. A vector as claimed in claim 8, which is a linear or circular DNA, a phage, a virus, a transposon, an IS element, a phasmid, a phagemid, a cosmid or a plasmid.
10. An organism comprising at least one nucleic acid sequence as claimed in claim 1, at least one nucleic acid construct as claimed in claim 6 or at least one vector as claimed in claim 8.
11. An organism as claimed in claim 10, which is a eukaryotic organism.
12. An organism as claimed in claim 10 or 11, which is a plant, a eukaryotic microorganism or an animal.
13. An organism as claimed in any of claims 10 to 12, which is a plant, a fungus or a yeast.
14. An organism as claimed in any of claims 10 to 13, which is *Yarrowia lypolytica* [sic], *Saccharomyces cereviseae* [sic], *Traustochytrium*, *Arabidopsis thaliana*, *Brassica napus* or *Linium* [sic] *usitatissimum*.

15. A transgenic plant comprising a nucleic acid sequence as claimed in claim 1 or a nucleic acid construct as claimed in claim 6.
- 5 16. A method of targeting proteins involved in lipid or fatty acid biosynthesis into liposomes or lipid bodies, which comprises combining the protein-encoding nucleic acids and one of the following sequences to give a joint protein-encoding sequence:
- 10 a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1,
- 15 b) nucleic acid sequences which are derived from the nucleic acid sequence shown in SEQ ID NO: 1 as the result of the degeneracy of the genetic code,
- 20 c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2 and which have at least 60% homology at the amino acid level,
- 25 d) a nucleic acid sequence with the sequence shown in SEQ ID NO: 3 or the amino-terminal portion of the coding region of this sequence, and
- and [sic] introducing the resulting sequence into a eukaryotic organism.
- 30 17. A method of targeting proteins involved in lipid or fatty acid biosynthesis into liposomes or lipid bodies, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct as claimed in claim 6 into an oil-producing organism.
- 35 18. A method of producing fatty acids or lipids, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct as claimed in claim 6 into an oil-producing organism, growing this organism
- 40 and isolating the oil contained in the organism.
19. A method of producing fatty acids, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct as claimed in
- 45 claim 6 into an oil-producing organism, growing this

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organism, isolating the oil contained in the organism and liberating the fatty acids.

20. A method as claimed in any of claims 16 to 19, wherein the
5 organism is a plant or a eukaryotic microorganism.

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